

FIGURE 1

TAAAACAGCTACAATATTCCAGGGCCAGTCACTGCCATTCTCATAACAGCGTCAGAGAGAAAGAACTGACTGA
AACGTTGAGATGAAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGTGCTGTTGGTTCCCAGTCTCTCA
AGACCAGGAACGAGAAAAAGAAGTATCAGTGACAGCGATGAATTAGCTTCAGGGTTTTGTGTTCCCTTACCC
ATATCCATTTCGCCCACTTCCACCAATTCCATTCCAAGATTCCATGGTTAGACGTAATTTCCTATTCCAAT
ACCTGAATCTGCCCTACAACCTCCCTTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCA
CCTGAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCCTGTTAATAAAAGAAAAACAAATGTAATTGAA
ATAGCACACAGCATTCTCTAGTCAATATCTTAGTGATCTCTTAATAAACATGAAAGCAAAGATTGGTTTC
TTAATTCCACA

FIGURE 2

GGAGAGAGGCAGCGCGGGTGAAAGGCGCATTGATGCAGCCTGCGGCGGCCCTGGAGCGCGCGAGCCAGACGCTG
ACCACGTTCCCTCCCTCGGTCTCCTCCGCCTCCAGCTCCGCGCTGCCCGGCAGCCGGAGCC**ATG**CGACCCCAGG
GCCCGCCGCCCTCCCCGAGCGGCTCCGCGCTCCTGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTGAGCG
CCTCTGAGATCCCCAAGGGGAAGCAAAGGGCGAGCTCCGGCAGAGGGGAGGTGGACCTGTATAATGGAATGT
GCTTACAAGGGCCAGCAGGAGTGCCTGGTCAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTGGGA
TCCCAGGTGGGATGGATTCAAAGGAGAAAAGGGGAATGTCAGGGAAAGCTTGAGGGAGTGTACATTACAA
ACTACAAGCAGTGTTCATGGAGTCATTGAATTATGGCATAGATCTGGAAAATTGCGAGTGTACATTACAA
AGATGCGTCAAAATAGTGCCTAACAGAGTTGTCAGTGGCTCACCGCTAAATGCAGAAATGCATGCTGTC
AGCGTTGGTATTCACATTCAATGGAGCTGAATGTCAGGACCTCTTCCATTGAAGCTATAATTATTGGAC
AAGGAAGCCCTGAAATGAATTCAACAATTAAATTACATCGCACTCTCTGTGGAAGGACTTGTGAAGGAATTG
GTGCTGGATTAGTGGATGTTGCTATCTGGGTGGCACTTGTTCAGATTACCCAAAAGGAGATGCTTCACTGGAT
GGAATTCACTTCGCATCATTATTGAAGAACTACCAAA**TAA**ATGCTTAATTTCATTGCTACCTCTTT
TTATTATGCCTTGAATGGTCACTAAATGACATTAAATAAGTTATGTATACATCTGAATGAAAAGCAAAG
CTAAATATGTTACAGACCAAGTGTGATTCACACTGTTAAATCTAGCATTATTCAATTGCTTCAATCAA
AAGTGGTTCAATATTTTTAGTTGGTTAGAATACCTTCATAGTCACATTCTCAACCTATAATTGGA
ATATTGTTGGTCTTTGTTCTTCTTAGTATAGCATTAAATAAAAGCTACCAATCTTGTAC
AATTGTAATGTTAAGAATTTTATCTGTTAAATAAAATTATTCCAACA

FIGURE 3

GCCAGGGGAAGAGGGTATCCGACCGGGGAAGGTCGCTGGCAGGGCGAGTTGGAAAGCGGCAGCCCCCGCCG
 CCCCCCGCAGCCCTTCTCCTCCTTCTCCCACGTCTATCTGCCTCTCGCTGGAGGCCAGGCCGTGCAGCATCGA
 AGACAGGAGGAAGTGGAGCCTCATGGCCGGCCGGGGCGCCGGCTCGGGCTTAAATAGGAGCTCCGGCTCTG
 GCTGGGACCCGACCGCTGCCGGCCGCTCCGCTGCTCCTGCCGGTGA**TG**AAAACCCAGCCGGCCGCC
 CCTGGCAAGGCCCTCGCCTCCTGCCACTCTGGCCAGTGGAGGCCAGACGGCCTTCCCAAGCA
 GTACCCCTGTTCCGCCCTGCGCAGTGGTCTCGCTGCTGGGGCCGCGCATAGCTCCGACTACAGCATGTG
 GAGGAAGAACAGTACGTCAACAGGCTGCGCAGTGGAGGCCAGGGCTGGCGAGGCGCTGGCGTGTGAAGGA
 GATCGAGGCGGGGGAGGCCTGCAGAGCGTGCACAGGGTGTTCGGCCGGCGTCCCCAGCGCACCG
 GCAGACGTCGGCGAGCTGGAGGTGCAGCGCAGGCACTCGCTGGCTCGTTGTGGTGCATCGTGCAGCCC
 CGACTGGTTCGTGGCGTGGACAGCCTGGACCTGTGCGACGGGACCGTTGGCGGGAAACAGCGCCGCTGGACCT
 GTACCCCTACGACGCCGGACGGACAGCGGCTCACCTCTCCCTCCCAACTCGCCACCATCCGCAGGACAC
 GGTGACCGAGATAACGTCTCCTCCAGCCACCCGCCAAGTCCACTACCCGCGCTGAAGGCCCTGCC
 TCCCACGCCAGGGTACACTGCTGCGCTGCGACAGAGCCCCAGGGCTTACCCCTCCGCCAGTCCTGCC
 CAGCAGGGACAATGAGATTGTAGACAGCGCCTCAGTCCAGAAACGCCGCTGGACTGCGAGGTCTCCCTGTGGTC
 GTCCCTGGGACTGTGCGGAGGCCACTGTGGGAGGCTCGGACCAAGAGCAGGACTCGCTACGTCCGGTCCAGCC
 CGCCAACAAACGGGAGCCCTGCCCGAGCTCGAAGAAGAGGCTGAGTGCCTGATAACTGCGCT**TAA**GACCA
 GAGCCCCCGCAGCCCTGGGGCCCCCGAGCCATGGGTGTCGGGCTCTGTGCAGGCTCATGCTGCAGGC
 CCGAGGGCACAGGGGTTTCGCGCTGCTCTGACCGCGTGAGGCCGCCACCATCTGCACTGAAGGCC
 TCTGGTGGCCGGCAGGGCATTGGAAACAGCCTCCTCTTCCAAACCTTGCCTTAGGGGCCCCGTGTCCC
 GTCTGCTCTCAGCCTCCTCCTGCAAGGATAAAAGTCATCCCCAAGGCTCCAGCTACTCTAAATTATGTCTCCTT
 ATAAGTTATTGCTGCTCCAGGAGATTGTCCTCATGTCAGGGCCTGGCTCCACGTGGTTGCAGATACTCA
 GACCTGGTGCCTAGGCTGTGCTGAGCCCACCTCCGAGGGCGCATCCAAGCAGGGCCACTTGAGAAGTGAAT
 AAATGGGGCGGTTTGGAAAGCGTCAGTGTTCATGTTATGGATCTCTGCGTTGAATAAGACTATCTCTGT
 TGCTCACAAAAAAAAAAAAAA

FIGURE 4

GAGGAACCTACCGGTACCGGCCGCGCTGGTAGTCGCCGGTGTGGCTGCACCTCACCAATCCGTCGCCGCC
CTGGGCCGTCGGAGAGTGCCTGCTCTCCTGCACGCCGTGCTTGGCTCGGCCAGGCCGGTCCGCCCA
GGTTTGAGGATGGGGAGTAGCTACAGGAAGCAGCCCCGCGATGGCAAGGTATATTGGAGTGGAAATGAAAAGA
AGTATTAGAAATGAGCTGAAGACCATTACAGATTATTTGGGACAGATTGTGATGCTGATTACCCCT
TGAAGTAATGAGACAGAAGTCTCAAATTGCATATTACACTGGAACCAGCAGTGAATCTTAAATGTTAAC
TTAAATCAGAACTTGCATAAGAAAAGAGA**AT**TGGAGCTGGTAAATAAGATGACTTATCAGAGACTTGAAAAG
GATCATTCTCTGTTCTGATAGTGTATGGCCATTAGTGGGACAGATCAGGATTTCAGTTACTTGG
AGTGTCCAAAAGTCAAGCAGTAGAGAAAATAAGACAAGCTTCAGAAGGATTGGCATTGAAGTTACATCCTGATAAA
AAACCCGAAATAACCCAAATGCACATGGCATTTTAAAAATAATAGAGCATATGAAGTACTCAAAGATGAAA
TCTACGGAAAAAGTATGACAAAATATGGAGAAAAGGGACTTGAGGATAATCAAGTGGCAGTGTGAAAGCTGAAA
CTATTATCGTTATGTTGGTATTGATGATGATCCTGAAATCATACATTGGAAAGAGAAATTGATG
TGCTGTTAATTCTGGAGAATGTGGTTGTTAAATTACTCCCCAGGCTGTTACACTGCCATGATTAGCTC
CACATGGAGAGACTTGTCAAGAAGTGGATGGGTTACTTCGAATTGGAGCTGTTACTGTGGTGTGATAGAATT
GCTTGCAGAATGAAAGGAGTCAACAGCTATCCCAGTCTTCATTTCGGTGGAATGGCCCAAGTGAAATA
TCATGGAGACAGATCAAAGGAGAGTTAGTGAAGTTGCAATGCAGCATGTTAGAAGTACAGTGACAGAACTTGT
GACAGGAAATTGTCACACTACAAACTGCTTGTGCTGGTATTGGCTGGCTGATCACTTTGTTCAA
AGGAGGAGATTGTTGACTTCACAGACAGACTCAGGCTTAGTGGCATGTTCTCAACTATTGGATGCTAA
AGAAATATAATTGGAAGTAATACATAATTCCAGATTGAAACTACTTCGGCAACACACTAGAGGATCGTT
GGCTCATCATCGGTGGCTGTTATTTCATTGGAAAAAAATGAAAATTCAAATGATCCTGAGCTGAAAAAAACT
AAAAACTCTACTTAAATAATGATCATATTCAAGTGGCAGGTTGACTGTTCTCTGCACAGACATCTGAGTAA
TCTGTATGTTTCAGCGTCTAGCAGTATTAAAGGACAAGGAACCAAAGAATATGAAATTCTCATCGGAA
GAAGATTCTATGATATACTTGCCTTGCCTTGGGAAAGAAGTGTGATTCTCATGTTACCGCTGGACCTCAA
TTTCTGCCAATGCAAAGAACCATGGCTTGTGATTCTTGCCTTGGGCTGTCAGGTTACAGATTGACAGTTCATG
ACCAGAGTTAACAGGATGATCAATCTCCTTATGGTCAGCTTAAGTTGGTACACTAGATTGACAGTTCATG
GGGACTCTGTAACATGTATAACATTAGGCTTACAGGCTTACAGGTTACCGTCAACATCATGAGTA
TGAAGGACATCACTGTGTAACAAATCTGGAGTTAGAGGATCTTATGAAATCTCAGTGGCTCCCTTAC
ACCCACACCTCAACGAACTAGTTACACAAAGAAAACACAAGTCTGGATGGTGTATTCTATTCTCCGG
GTGTCATCCTTGCAAGTCTTAATGCCAGAATGGAAAAGAATGGCCCGGACATTAACGGACTGATCAACGTGG
CAGTATAGATTGCCAACAGTATCATTCTTGTGCCAGGAAACGTTAAAGATACCTGAGATAAGATT
TCCCCAAAATCAAATAAGCTTACAGTATCACAGTTACATGGTGAATAGGGATGCTTATTCCCTGAGAAT
CTGGGGCTAGGATTTCACCTCAAGTATCCACAGATCTAACACCTCAGACTTCACTGAAAAAGTCTACAAGG
AAAAAATCATGGGTGATTGATTCTATGTCCTGGTGTGGACCTGCCAGAATTGCTCCAGAATTGAGCT
CTTGGCTAGGATGTTAAAGGAAAAGTGAAGGCTGGAAAAGTAGACTGTCAGGCTTATGTCAGACATGCCAGAA
AGCTGGGATCAGGGCTATCCAACGTGTTAGTTTACAGGAAAGAGCAGGAAAGAGAAATTCTCAAAGAGGCA
GATAAAATACAGAGATGCAAAGAACATCGCTGCCCTAAATAGTAAAAATTGAAAACCTCCGAAATCAAGGCAA
GAGGAATAGGATGAACT**TGA**ATATTGTAAGGATGAAAAGTAAAGGAAATTCTGACAGATGACATCAG
AAGCACACATTAGAATGTTACATTATGATGGGAATGAATGAAACATTATCTTAGACTGTCAGTTGACTGCA
GAAATTATCTACAGCAGTGTGTTAAAGAAGGGCTGCAAAACTTTCTGTAAAGGGCCGTTATAAATATT
GACTTTGCAGGCTATAATATGGTTCACACATGAGAACAGAATAGAGTCATCATGTATTGTTATTGCT
TTAACACCTTAAATAATTAAACGATTCTTAGCTCAGGCCATACAAAGTAGGCTGGATTCACTGCT
GACCATAGATTGCTGCCCTCGACGGACTTAAATGTTCAGGTGGCTGGCTGAACATGAGTCGCTGTGCT
ATCTACATAATGCTAAGTTGATGAAAGTCCACCTTCCCTCACGTTTGTGACCTGAAAAGAGGTAAC
TAGTTTGGTCACTGTTCTCTAAATGCTACCTAACCATATATTATTCGTTTAAACACCCAT
GATGTGGCACAGTAAACAAACCTGTTATGCTGATTATTAGAGGAGATTCTCATTGTTTCTTCCCTCA
AAGGTTGAAAAAAATGCTTTAAATTTCACAGGCCAGAAGAACAGTGCAGCAGTATATGTCACACAGTAAGTACAC
AAATTGAGCAACAGTAAAGTGCACAAATTCTGTAGTTGCTGTATCATCCAGGAAACCTGAGGGAAAAAAATT
TAGCAATTAACTGGGCACTGTGAGTAGTCTAAATGTTACAGTATTAGGTTAGGTTCTATATTAAAGATATA
TGTGTTCACTGTTCTGAAATTGTTCTAGAAATTCTCCAGTGTGATTGTTGAGGCTCATCTAAT
TTACATATTGCTCTGAACTTGTGTTCTAGAAATTCTGTTGACCTGTATCTTATTACATGGGTTTCTTCT
TTTTCTCTGTCAGTCTATTATTCAATAGGAAAATTACTTACAGGTTGTTTACTGTTAGCT
AATGATACTGAGTTATTCCAGTTACTGTTACTGTGAGGGCTGCCCTTTCAGATAAAATTGACATAATA
ACTGAAGTTATTGTTATAAGAAAATCAAGTATATAAATCTAGGAAAGGGATCTCTAGTTCTGTGTTAGA
CTCAAAGAATCACAAATTGTCAGTAACATGTTAGTTAGTTAATTCTAGGTTGACAGAATGGTAAAAA
CCAATCAGTAAAAGAGGTCATGAATTAAAGGCTGCAACTTTCTCAAAAAAAAAAAAAAA

FIGURE 5

GGCAACATGGCTCAGCAGGTTGCCAGAGCCATGGCAAAGAATGGACTTGTAATTGCATCCTGGTATCACC
 TTACTCCTGGACCAGACCACAGCCACACATCCAGATTAAAAGCCAGGAAGCACAGCAAACGTCGAGTGAGAGAC
 AAGGATGGAGATCTGAAGACTCAAATTGAAAAGCTCTGGACAGAACGTCATGCCTGAAGGAAATTCAAGCCCTG
 CAGACAGTCTGTCTCGAGGCCTAAAGTCACAAGAAATGCTACCTTGCTCAGAAGGTTGAAGCATTCCAT
 GAGGCCAATGAAGACTGCATTCCAAGGAGGAATCCTGGTTATCCCCAGGAACCTCGACGAAATCAACGCCCTC
 CAAGACTATGGTAAAGGAGCCTGCCAGGTGTCATGACTTTGGCTGGCATCAATGACATGGTCACGGAAAGGC
 AAGTTGTTGACGTCAACGGAATCGCTATCTCCTCCTCAACTGGGACCGTGACAGCCTAACGGTGGCAAGCGA
 GAAAAGTGTGTCCTGTTCTCCAATCAGCTCAGGGCAAGTGGAGTGATGAGGCCTGTCGACAGCAAGAGATAAC
 ATATGCGAGTTCACCATCCCTAATAGGTCTTCTCCAATGTCCTCCAAGCAAGATTCACTATAACTTATAGG
 TTCATGATCTCTAAGATCAAGTAAAATCATATTAACTTATTAAAAAATTGCAACACAAGATCAATGTCCAT
 AGCAATATGATAGCATCAGCAATTGGCTAACACATTCTTGGGATTTGCCCTCCTGGGTATAGGGGATC
 AGAAATATTGATCCATGTCACGCAGATAAAATGGCTCTGCTAACAGACTAAAATCTTCTCTAGTCTTTC
 TCACTTGTACAAACCCAGTTGTTCAAAAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTT
 AGGCTACCTGAAAGATTCCCTTGAAGTTAGCGTATGTTGACTAACAAAATTCCCTACATCAGAGACTCT
 AGGTGCTATATAATCCAAAATTTTCAAGCCTGCTCATTCTGCTCCATGCTGGCAATAATACCTTGTCAAGCC
 CATTACCTTATTTGAATTGCTCCATCTCCTGGTGGACTGTATCTGCTGCCATATCAGAACACAAACCC
 TGAAGAGGTTCTGATTTGATTTTTTCTTCATGCTAACCTTTTGAAGTTCCAGGCCAATTG
 AATGAAATGACAAGGTGTATATTGATCAATTTCATTCCCACCATGCAATTACACCTCTAACATTAAATGGGTA
 ACCCTAAGGCATATCAAAGAAGCAGATTGCAATGATAAACGGAAATAGAAAAAAGAACCTACATTATTGCTT
 TAGCATCCTTACTCTCACCTTATGAGATTGAGAGTGGACTTACATTCCCTTTACATTTCGTATATT
 TTTTTTAGCCATCATTATGTTAAGTCTATTATGGCAACCAATCTTGAAGCTGAAACTGAATTAAAG
 AATGCTATCTGGAAAATTGCAACGTCTGTCAATTTCATTGCTTAGTGGAGGGAAATGGGCTTTAGAAG
 CAAACAATTAAATATTGTTCTCAAATAATAGTGTAAACATTGAATGTGTTGTGAACAATATCC
 CACTTGCAAACCTTAACACATGCTGGAAATTAGTTAGCTGTTTCAATTGCTCAATAATAAGCCTGAA
 TTCTGATCAATAAAAAAAAAAAAAAA

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FIGURE 6

MKKVLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPFRPLPPIPFPFRFWFRRNFPPIPES
APTTPLPSEK

Signal sequence.

amino acids 1-17

FIGURE 7

MRPQGPAA SPQR LRG LLLL LQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGVPG RDGSPGANVIP
GTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIAECTFTKMRSNSALRVLFSGSLRLKCR
NACCQRWYFTFNGAECSGPLPIEAIITYLDQGSPEMNSTINIHRRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGD
ASTGWNSVSRIIIIEELPK

Signal sequence.

amino acids 1-30

N-glycosylation site.

amino acids 186-189

N-myristoylation sites.

amino acids 67-72, 117-122, 163-168, 199-204, 203-208

FIGURE 8

MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQTAFPKQYPLFRPPAQWSSLGA
AHSSDYSMWRKNQYVSNGLRDFAERGEAWALMKEIEAAGEALQSVHEVFSAPAVPSGTGQTSAELEVQRRHSLVS
FVVRIVPSPDWFGVDSLDLCDGDRWREQAALDLYPYDAGTDSGFTFSSPNFATIPQDTVTEITSSSPSHPANSF
YYPRLKALPPIARVTLLRLRQSPRAFIAPPAPVLPSPRDNIEVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKS
RTRYVRVQ PANNGSPCPELEEEAECVPDNCV

Signal sequence.

amino acids 1-26

Glycosaminoglycan attachment site.

amino acids 131-134

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 144-147

N-myristoylation sites.

amino acids 26-31, 74-79, 132-137, 134-139, 190-195, 287-292, 290-295

FIGURE 9

MGVWLNKDDYIRDILKRIILCFLIVYMAILVGTQDFYSILLGVSKTASSREIRQAFKKLALKLHPDKNPNNPNAHG
 DFLKINRAYEVLKDEDLRKKYDKYGEKGLEDNQGGQYESWNYYRYDFGIYDDDPEIITLERREFDAAVNSGELWF
 VNFYSPGCSHCHDLAPTWRFAKEVDGLLIGAVNCGDRMLCRMKGVSYPRLFIFRSGMAPVKYHGDRSKESEL
 VSFAMQHVRSTVTELWTGNFVNLSIQTAFAGIGWLITFCSKGGDCITSQTRLRLSGMLFILNSLDAKEIYLEVIHN
 LPDFELLSANTLEDRLAHHRWLLFFHFGKNENSNDPELKKLKTLLKNDHIQVGRFDCSSAPDICSNLVFQPSILA
 VFKGQGTKEYEIHGKKILYDILAFAKESVNHSVTTLGPQNFPANDKEPWLVDFFAPWCPCRALLPELRRASNL
 LYGQLKFGTLDCTVHEGLCNMYNIQAYPTTVFNQSNIHEYEGHHSAEQILEFIEDLMNPSVSLTPTTFNELVT
 QRKHNEVWMVDFYSPWCHPCQVLMPEWKRMARTLTGLINVGSIDCQQYHSFCAQENVQRYPEIRFFPKSNKAYQ
 YHSYNGWNRDAYSRLRIWGLGFLPQVSTDLPQTFSEKVILQGKNHWIDFYAPWCGPCQNFAPFELLARMIKGKV
 KAGKVDCQAYAQTCQKAGIRAYPTVKFYFYERAKRNFQEEQINTRDAKAIAALISEKLETLRNQGKRNKDEL

Signal sequence.

amino acids 1-48

N-glycosylation site.

amino acids 484-487

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 445-448

N-myristoylation sites.amino acids 2-7, 41-46, 103-108, 110-115, 157-162, 182-187, 243-248, 458-463,
 566-571**Amidation sites.**

amino acids 389-392, 739-742

Endoplasmic reticulum targeting sequence.

amino acids 744-748

Cytochrome c family heme-binding site signature.

amino acids 158-163

Thioredoxin.

amino acids 128-234, 406-509, 511-592, 623-703

DnaJ domain.

amino acids 35-100

FIGURE 10

MAQQACPRAMA~~K~~NGLVICILVITLLL~~D~~QTTSH~~S~~RLKARKHSKRRVRDKDGDLKTQIEKLWTEVNALKEIQALQT
VCLRGTKVHKKC~~Y~~LASEGLKH~~F~~HEANEDCISKG~~G~~GILV~~I~~PRNSDEINALQDYGKRSLPGVNDFWLGINDMVTEGKF
VDVNGIAISFLNWDR~~A~~QPNGGKREN~~C~~VLF~~S~~QSAQGKWSDEACRSSKRYICEFTI~~P~~K

Signal peptide.

amino acids 1-31

N-myristoylation sites.

amino acids 14-20, 155-161

Amidation sites.

amino acids 126-130, 170-174

C-type lectin domain signature.

amino acids 176-201